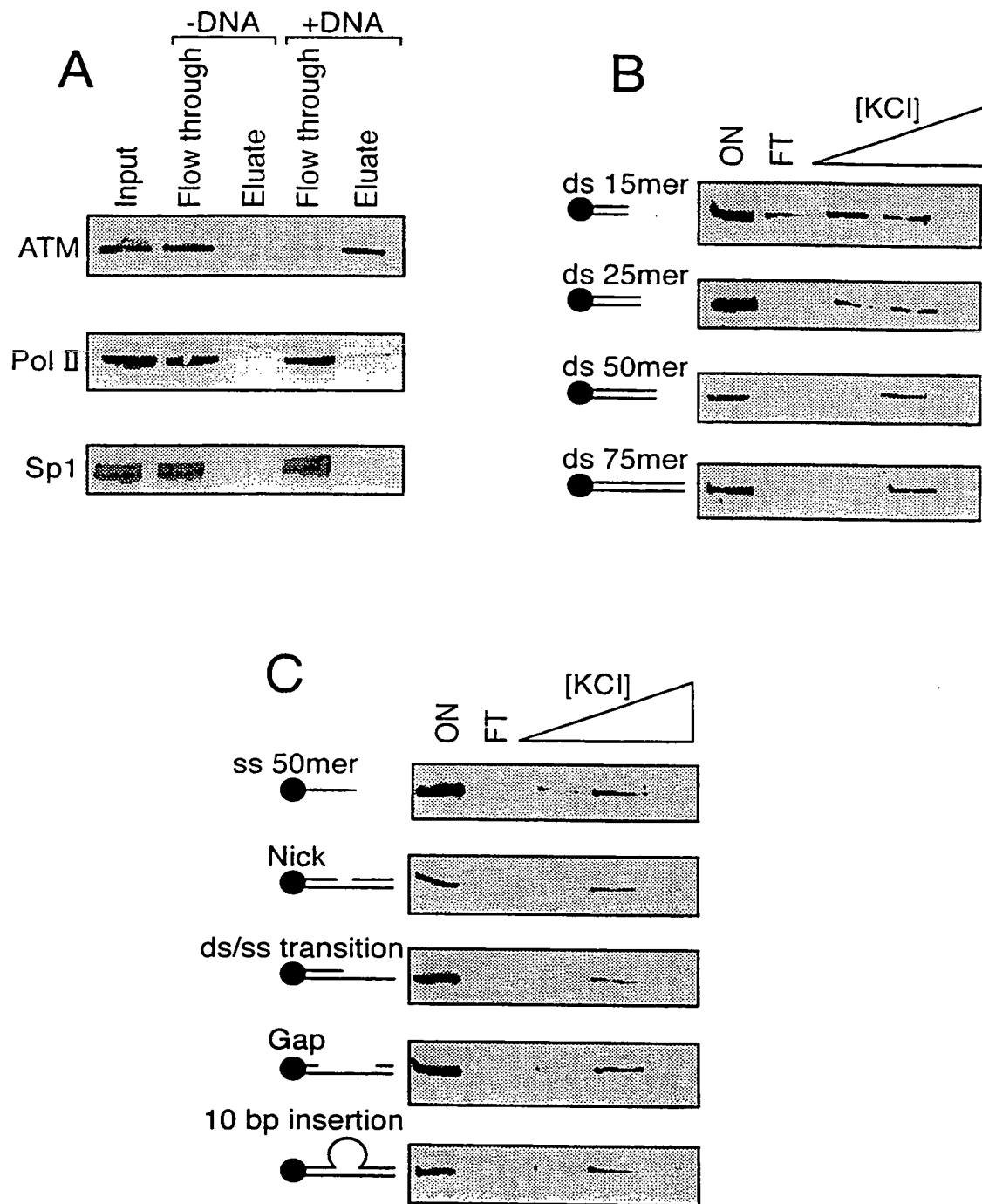


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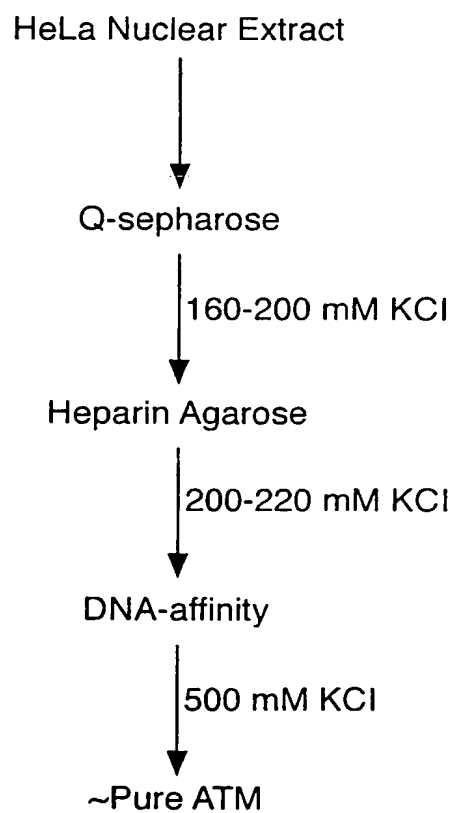
Fig.1.



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Fig.2.

A



B

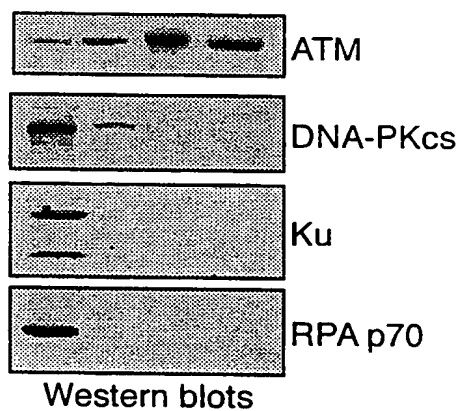
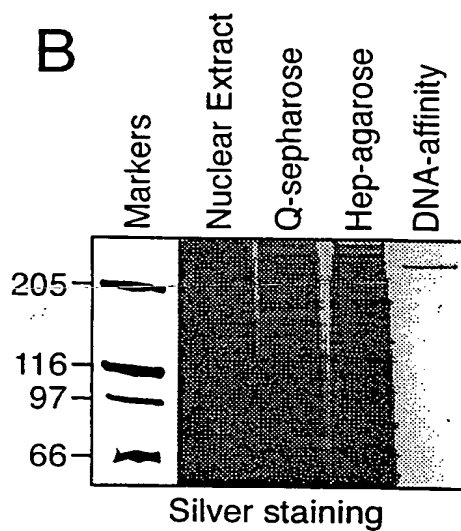
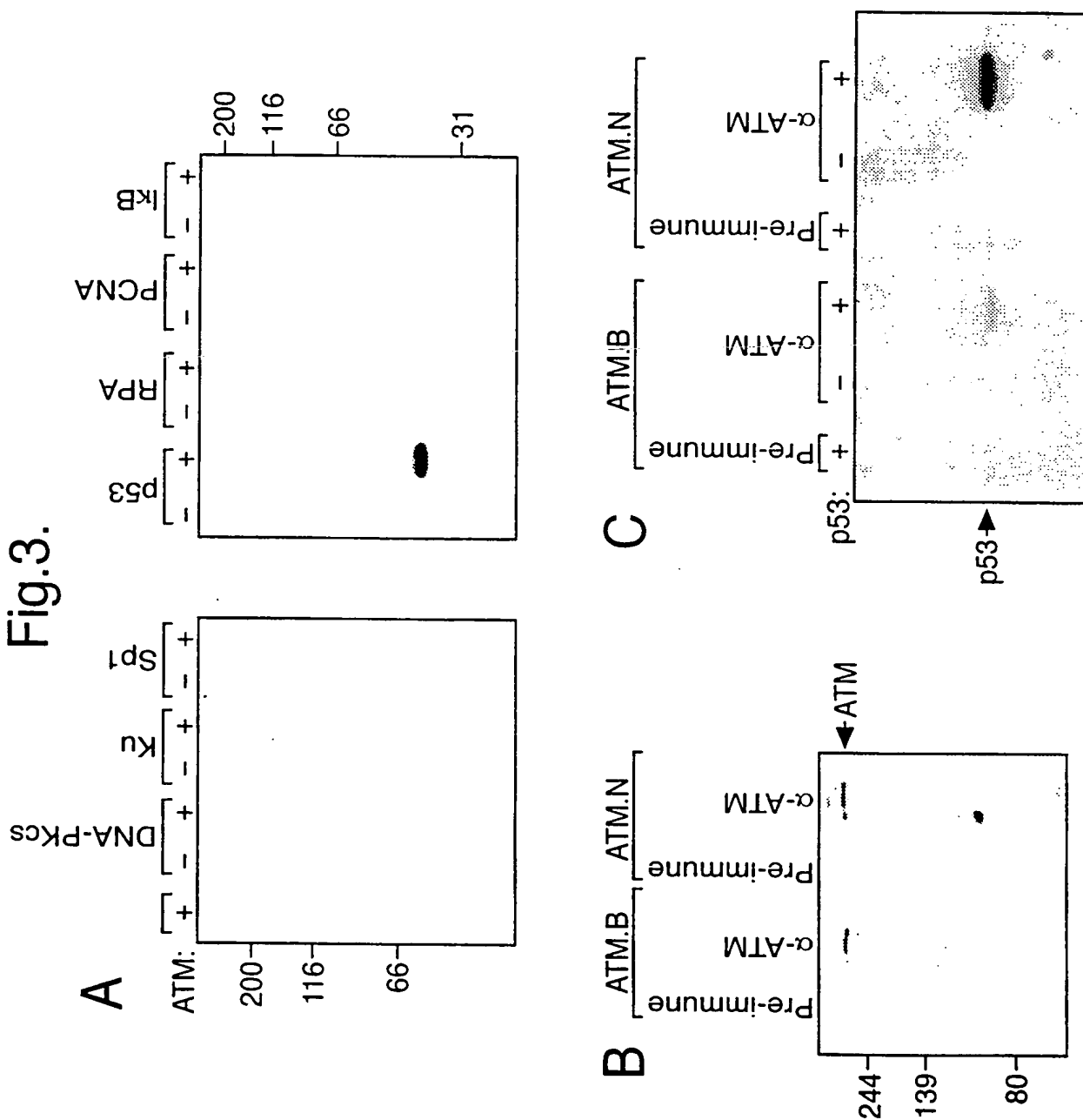
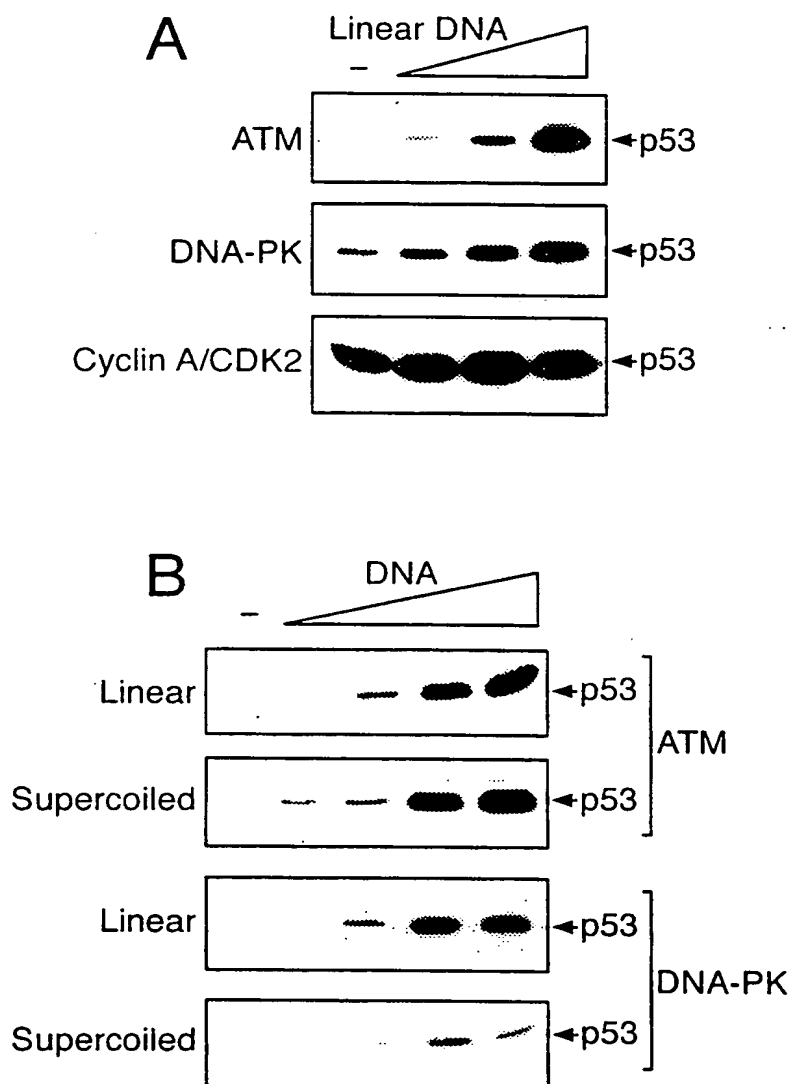


Fig.3.



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Fig.4.



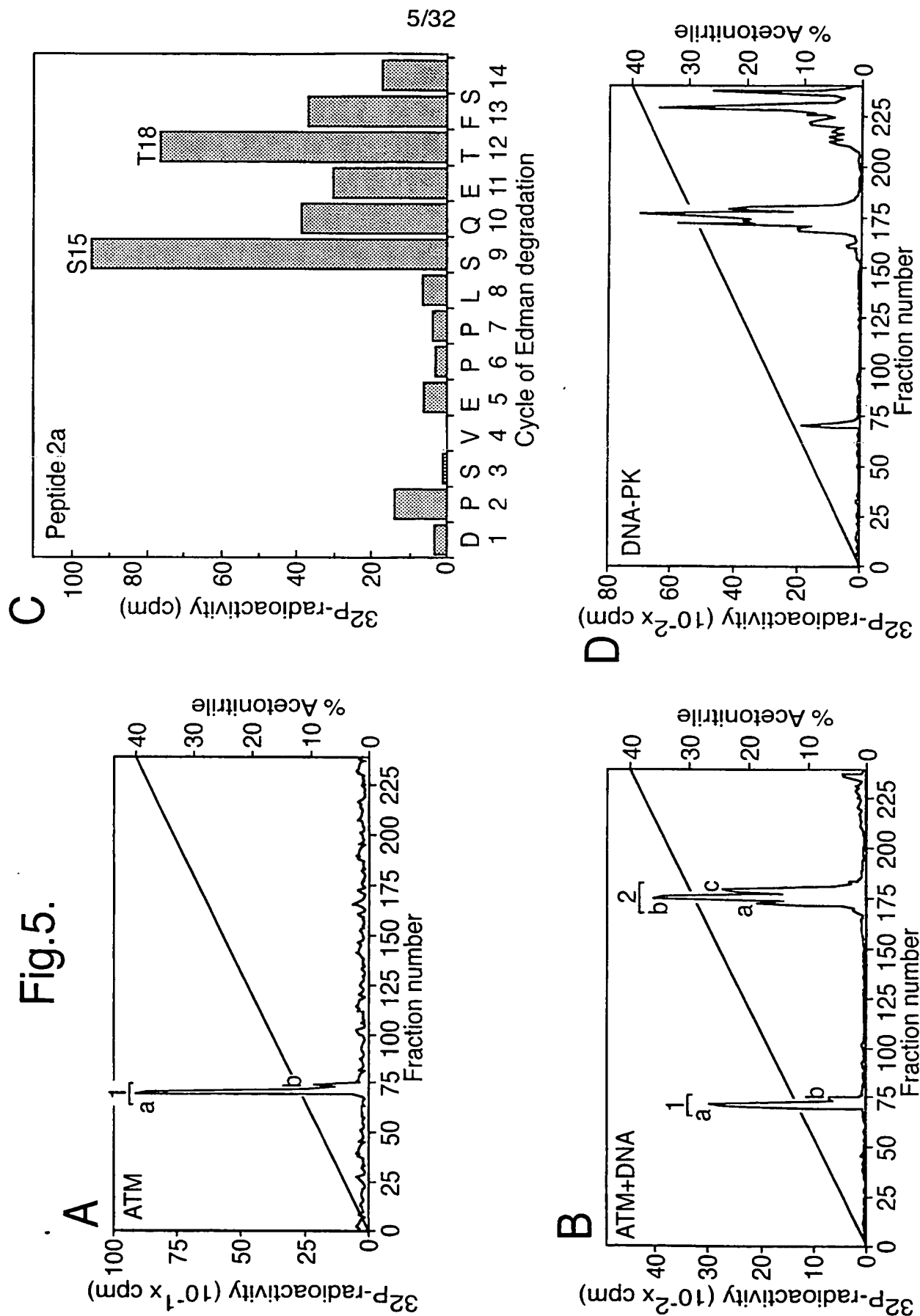


Figure 6a

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Figure 6b (11)

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Figure 6 b (111)

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Figure 6b (1v)

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3701 AGGCTTTGTT TGCCCTGTGT AAATCTGTGA AAGAGAATGG ATTAGAACCT
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Figure 6b (v)

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Figure 6b (v1)

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7751 ACCAATTGGC TGCTAGAATG GGGACCAAGA TGATGGGAGG CCTAGGATTT
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Figure 6b (vii)

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9051 TGATCCACTC TTTGACTGGA CCATGAATCC TTTGAAAGCT TTGTATTTAC
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Figure 7a

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FT                               KQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEP
FT                               PEVGSDCTTIHNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRD
FT                               RRTEENLRKKGEPHHELPPGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEM
FT                               FRELNEALELKDAQAGKEPGGSAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD"
XX
SQ   Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 other;

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M14695 Length: 1303 July 10, 1998 12:29 Type: N Check: 4902 ..

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101 ACTGCCTTCC GGGTCACTGC CATGGAGGAG CCGCAGTCAG ATCCTAGCGT
151 CGAGCCCCCT CTGAGTCAGG AAACATTTTC AGACCTATGG AAATACTTTC
201 CTGAAAACAA CGTTCTGTCC CCCTTGCCGT CCCAAGCAAT GGATGATTTG
251 ATGCTGTCCC CGGACGATAT TGAACAAATGG TTCACTGAAG ACCCAGGTCC

```

Figure 7b (1)

Figure 7b (11)

301 AGATGAAGCT CCCAGAATGC CAGAGGCTGC TCCCCCGTG GCCCCCTGCAC
351 CAGCGACTCC TACACCGGCG GCCCCCTGCAC CAGCCCCCTC CTGGCCCCCTG
401 TCATCTTCTG TCCCTTCCCA GAAAACCTAC CAGGGCAGCT ACGGTTTCCG
451 TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT
501 CCCCTGCCCT CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG
551 CAGCTGTGGG TTGATTCCAC ACCCCCGCCC GGCACCCGCG TCCGCGCCAT
601 GGCCATCTAC AAGCAGTCAC AGCACATGAC GGAGGTTGTG AGGCGCTGCC
651 CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC TCCTCAGCAT
701 CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA
751 CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT
801 CTGACTGTAC CACCATCCAC TACAACCTACA TGTGTAACAG TTCTGTCATG
851 GGCGGCATGA ACCGGAGGCC CATCCTCACC ATCATCACAC TGAAGACTC
901 CAGTGTAAT CTACTGGGAC GGAACAGCTT TGAGGTGCGT GTTTGTGCCT
951 GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG CAAGAAAGGG
1001 GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA
1051 CAACACCAGC TCCTCTCCCC AGCCAAAGAA GAAACCACTG GATGGAGAAT
1101 ATTTACCCCT TCAGATCCGT GGGCGTGAGC GCTTCGAGAT GTTCCGAGAG
1151 CTGAATGAGG CCTTGGAACCT CAAGGATGCC CAGGCTGGGA AGGAGCCAGG
1201 GGGGAGCAGG GCTCACTCCA GCCACCTGAA GTCCAAAAAG GGTCAGTCTA
1251 CCTCCCGCCA TAAAAAACTC ATGTTCAAGA CAGAAGGGCC TGA CTCAGAC
1301 TGA

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Figure 8a (i)

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!!NA_SEQUENCE 1.0
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XX
NI   g1235901
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DT   20-MAY-1996 (Rel. 47, Last updated, Version 1)
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-> DE   Human FRAP-related protein (FRP1) mRNA, complete cds.
XX
KW
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-8210
RA   Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L.;
RT   "cDNA cloning and gene mapping of a candidate human cell cycle
RT   checkpoint protein";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:2850-2855(1996).
XX
RN   [2]
RP   1-8210
RA   Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L.;
RT   ;
RL   Submitted (22-FEB-1996) to the EMBL/GenBank/DDBJ databases.
RL   Karlene A. Cimprich, Chemistry, Harvard University, 12 Oxford Street,
RL   Cambridge, MA 02138, USA
XX
DR   SPTREMBL; Q13535; Q13535.
XX
FH   Key          Location/Qualifiers
FH
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FT                   /chromosome="3"
FT                   /cell_type="Jurkat T-cell"
FT                   /map="3q22-q24"
FT   CDS              106. .8040
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FT                   /db_xref="SPTREMBL:Q13535"
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FT                   /product="FRAP-related protein"
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FT                   TDVNVVAVELVKKITDSQPTSVMLLDFIQHIMKSSPLMFVNVSGSHEAKGSCIEFSNWII
FT                   TRLLRIAATPSCHLLHKKICEVICSLFLFKSKSPAIFGVLTKEQLQFEDLVYLHRRN
FT                   VMGHAVEWFPVMSRFLSQLDEHMGYLOSAPIQLMSMONLEFIEVTLLMVLTRI IATVFF
FT                   RRQELLLWQIGCVLLEYGSPKIKSLAISFLTFLQGLPAQPASTFFSFLLELLKHLV
FT                   EMDTDQLKLYEPEPLSKLIKTLFPFEAEAYRNIEPVYLANMLLEKLCVMFEDGVLMRLKSD
FT                   LLKAALCHLLQYFLKFVPAGYESALQVRKVYVRNICKALLDVLGIEVDAEYLLGPLYAA
FT                   LKMESEMEIEEIQCQTQENLSSNSDGISPKRRRLSSSLNPSKRAPKQTEELKHVDMNQ
FT                   KSILWSALKQKAESLQISLEYSGLKNPVIEMLEGIADVVLQLTALCTVHCSHQNMNCRTF
FT                   KDCQHKSKKKPSVVTIWMSLDFYTKVLKSCRSLLSESVQKLDLEATIDKVVKIYDALIYM
FT                   QVNSSFEDHILEDLCGMLSLEPWIYSHSDDGCLKLTTFANLLTLSCRISDSYSPOAQR
FT                   CVFLLTLFPRIIFLEWRTAVYNWALQSSHEVIRASCVSFGFFILLQQQNSCNRVKILID
FT                   KVKDDSDIVKKEFASILGQLVCTLHGMFYLTSSLTEPFSEGHVDLFCRNKATSQHEC
FT                   SSSQLKASVCKPFLFLLKKKIPSPVKLAFIDNLHHLCKHLDFREDETQVKAIVLGLLNL
FT                   MEDPDKDVRVAFSGNIKHILESLSDEDFIKELFVLRMKEAYTHAQISRNNELKDTLLIL
FT                   TTGDIGRAAKGDLVPFALLHLHCLLSKKSASVSGAAYTEIRALVAKSVKIQSFFSQYK
FT                   KPICQFLVESLHSSQMTALPNTPCQNAQDVRKQDVAHQREMAFNLTSEIANVDFDFDLNR
FT                   FLTRTLQVLLPDLAASKASPAASALIRTLGKQLNVNRREILINNFKYIFSHLVCSCSKDE

```

Figure 8a (11)

FT LERALHYLKNETEIELGSLLRQDFQGLHNE LLRIGEHYQQVFNGLSILASFASSDDPY
 FT QGPRDIISPELMADYLOPKLLGILAFFNMQLLSSSVGIEDKKMALNSLSMLKLMGPKH
 FT VSSVRVKMMTTTLRTGLRFKDDFPELCCRAWDCFVRCLDHACLSLLSHVIVALLPLIHI
 FT QPKETAAIFHYLI IENRDAVQDFLHEIYFLPDHPELKKIKAVLQEYRKETSESTDLQTT
 FT LQLSMKAIQHENVDRRIHALTSLKETLYKNQEKLIKATDSETVEPIISQLVTVLLKGC
 FT QDANSQARLLCGECLGELGAIDPGRLDFTTETQGKDFTFVTGVEDSSFAYGLLMELTR
 FT AYLAYADNSRAQDSAAAYAIQELLSIYDCREMETNGPGHQLWRRFPHEVREILEPHLNTR
 FT YKSSQKSTDWSGVKKPIYLSKLGSNFAEWSASWAGYLITKVRHDLASKIFTCCSIMMKH
 FT DFKVTIYLLPHILVYVLLGCNQEDQOEYAEIMAVLKHDDQHTINTQDIASDLQQLSTQ
 FT TVFSMLDHLTQWARHKFQALKAKECPSKSNRNKVDMSVSTVDYEDYQSVTRFLDLIPQ
 FT DTLAVASFRSKAYTRAVMHFESFITEKKQNIQEHLGFLQKLYAMHEPDGVAGVSAIRK
 FT AEPSLKEQILEHESLGLLRDATAICYDRAIQLEPDQIIHYHGVVKSMLGLGQLSTVITQV
 FT NGVHANRSEWTDELNTYRVEAAWKL SOWDLVENYLAADGKSTTWSVRLGQLLLS AKKRD
 FT ITAFYDSLKLVR AEQIVPLSAASFERSYQRGY EYIVRLHMLCEHSIKPLFQHSPGD
 FT SSQEDSLNWVARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGECLWQSARVARK
 FT AGHHQTAYNALLNAGESRLAELYVERAKWLWSKGDVHQA LVLQKVELCFPENETPPE
 FT GKNNMLIHGRAMLLVGRFMEETANFESNAIMKKYKDVTA CLPEWEDGHFYLA KY YDKLMP
 FT MVTDNKMEKQGD LIRYIVLHFG RSLQYGNQFIYQSMPRMLTLWL DYGTKAYEWKAGRS
 FT DRVQMRNDLGKINKVITEHTNYLAPYQFLTA FSQ LISRICSHDEVFV LMEIIAKVFL
 FT AYPQQAMMMMTAVSKSSYPMRVNRCKEILNKA IHMKKSLEKFVGDATRLTDK LLELCNK
 FT PVDGSSSTLSMSTHFMLKKLV EEA TFSEILIP LQSVMIPTLPSILGTHANHASHEPFP
 FT GHWAYIAGFDDMVEILASLQKPKKISLKGSDGKFYIMMCKPKDDL RKCRLMEFNSLIN
 FT KCLRKDAESRRRELHIRTAVIPLNDEC GII EWVNNTAGLRPILTKLYKEGVYMTGKE
 FT LRQCM LPKSAALSEKLVFRE FLLPRHPPIFHEWFLRTFPDPTS WYSSRSAYCRSTAVM
 FT SMVGYILGLGDRHGENILFDSL TGECVHVDFNCLFNKGETFEVPEIVPFR LTHNMVNGM
 FT GPMGT EGLFR RACEVTMRLMRDQREPLMSVLKTF LHDPLV EWSKPVKGHSKAPLNETGE
 FT VVNEKAKTHVLDIEQRLQGVIKTRNRVTGLPLSIEGHVHYLIQEATDENLLCQMYLGWT
 FT PYM*
 XX
 SQ Sequence 8210 BP; 2511 A; 1555 C; 1738 G; 2406 T; 0 other;

U49844 Length: 8210 July 10, 1998 12:08 Type: N Check: 4511 ..

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 51 TGGAGACGCC GGAACCCGC GTTGGCGTGG TTGACTAGTG CCTCGCAGCC
 101 TCAGCATGGG GGAACATGGC CTGGAGCTGG CTTCCATGAT CCCC GCCCTG
 151 CGGGAGCTGG GCAGTGCCAC ACCAGAGGAA TATAATACAG TTGTACAGAA
 201 GCCAAGACAA ATTCTGTGTC AATTCATIGA CCGGATACTT ACAGATGTAA
 251 ATGTTGTTGC TGTAGAACTT GTAAAGAAAA CTGACTCTCA GCCAACCTCC
 301 GTGATGTTGC TTGATTTTCAT CCAGCATATC ATGAAATCCT CCCC ACTTAT
 351 GTTTGTAAAT GTGAGTGGAA GCCATGAGGC CAAAGGCAGT TGTATTGAAT
 401 TCAGTAATTG GATCATAACG AGACTTCTGC GGATTGCAGC AACTCCCTCC
 451 TGTCAATTTGT TACACAAGAA AATCTGTGAA GTCATCTGTT CATTATTATT
 501 TCTTTTTTAAA AGCAAGAGTC CTGCTATTTT TGGGGTACTC ACAAAGAAT
 551 TATTACAAC TTTTGAAGAC TTGGTTTACC TCCATAGAAG AAATGTGATG
 601 GGTCA TGCTG TGGAA TGCC AGTGGTCATG AGCCGATTTT TAAGTCAATT
 651 AGATGAACAC ATGGGATATT TACAATCAGC TCCTTTGCAG TTGATGAGTA
 701 TGCAAAATTT AGAATTTATT GAAGTCACTT TATTAATGGT TCTTACTOGT
 751 ATTATTGCAA TTGTGTTTTT TAGAAGGCAA GAACTCTTAC TTTGGCAGAT
 801 AGGTTGTGTT CTGCTAGAGT ATGGTAGTCC AAAAAATTAAA TCCCTAGCAA

Figure 8b(1)

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Figure 8b (ii)

851 TTAGCTTTTT AACAGAACTT TTTCAGCTTG GAGGACTACC AGCACAACCA
901 GCTAGCACTT TTTTCAGCTC ATTTTGGAA TTATTAAAAC ACCTTGTAGA
951 AATGGATACT GACCAATTGA AACTCTATGA AGAGCCATTA TCAAAGCTGA
1001 TAAAGACACT ATTTCCCTTT GAAGCAGAAG CTTATAGAAA TATTGAACCT
1051 GTCTATTTAA ATATGCTGCT GGAAAACTC TGTGTCATGT TTGAAGACGG
1101 TGTGCTCATG CGGCTTAAGT CTGATTTGCT AAAAGCAGCT TTGTGCCATT
1151 TACTGCAGTA TTTCCCTTAA TTTGTGCCAG CTGGGTATGA ATCTGCTTTA
1201 CAAGTCAGGA AGGTCTATGT GAGAAATATT GTTAAAGCTC TTTTGGATGT
1251 GCTTGGAATT GAGGTAGATG CAGAGTACTT GTTGGGCCCA CTTTATGCAG
1301 CTTTGAAAAT GGAAAGTATG GAAATCATTG AGGAGATTCA ATGCCAACT
1351 CAACAGGAAA ACCTCAGCAG TAATAGTGAT GGAATATCAC CCAAAGGCG
1401 TCGTCTCAGC TCGTCTCTAA ACCCTTCTAA AAGAGCACCA AACAGACTG
1451 AGGAAATTAA ACATGTGGAC ATGAACCAAA AGAGCATATT ATGGAGTGCA
1501 CTGAAACAGA AAGCTGAATC CCTTCAGATT TCCCTTGAAT ACAGTGGCCT
1551 AAAGAATCCT GTTATTGAGA TGTTAGAAGG AATTGCTGTT GTCTTACAAC
1601 TGA CTGCTCT GTGTACTGTT CATTGTCTC ATCAAAACAT GAACTGCCGT
1651 ACTTTCAAGG ACTGTCAACA TAAATCCAAG AAGAAACCTT CTGTAGTGAT
1701 AACTTGGATG TCATTGGATT TTTACACAAA AGTGCTTAAG AGCTGTAGAA
1751 GTTTGTTAGA ATCTGTTTCA AACTGGACC TGGAGGCAAC CATTGATAAG
1801 GTGGTGAAAA TTTATGATGC TTTGATTTAT ATGCAAGTAA ACAGTTCATT
1851 TGAAGATCAT ATCCTGGAAG ATTTATGTGG TATGCTCTCA CTTCCATGGA
1901 TTTATTCCCA TTCTGATGAT GGCTGTTTAA AGTTGACCAC ATTTGCCGCT
1951 AATCTTCTAA CATTAGCTG TAGGATTTCA GATAGCTATT CACCACAGGC
2001 ACAATCACGA TGTGTGTTT TTTCTGACTCT GTTTCCAAGA AGAATATTCC
2051 TTGAGTGGAG AACAGCAGTT TACAACCTGG CCCTGCAGAG CTCCCATGAA
2101 GTAATCCGGG CTAGTTGTGT TAGTGGATTT TTTATCTTAT TGCAGCAGCA
2151 GAATTCCTGT AACAGAGTTC CCAAGATTCT TATAGATAAA GTCAAAGATG
2201 ATTCTGACAT TGTCAAGAAA GAATTTGCTT CTATACTTGG TCAACTTGTC
2251 TGTACTCTTC ACGGCATGTT TTATCTGACA AGTTCTTTAA CAGAACCTTT
2301 CTCTGAACAC GGACATGTGG ACCTCTCTG TAGGAACCTG AAAGCCACTT
2351 CTCAACATGA ATGTTTATCT TCTCAACTAA AAGCTTCTGT CTGCAAGCCA
2401 TTCTTTTCC TACTGAAAAA AAAATACCT AGTCCAGTAA AACTTGCTTT
2451 CATAGATAAT CTACATCATC TTTGTAAGCA TCTTGATTTT AGAGAAGATG
2501 AAACAGATGT AAAAGCAGTT CTTGGAACCT TATTAAATTT AATGGAAGAT

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Figure 8b (111)

2551 CCAGACAAAG ATGTTAGAGT GGCTTTTAGT GGAAATATCA AGCACATATT
2601 GGAATCCTTG GACTCTGAAG ATGGATTAT AAAGGAGCTT TTTGTCTTAA
2651 GAATGAAGGA AGCATATACA CATGCCCAA TATCAAGAAA TAATGAGCTG
2701 AAGGATACCT TGATTCCTAC AACAGGGGAT ATTGGAAGGG CCGCAAAAGG
2751 AGATTTGGTA CCATTTGCAC TCTTACACTT ATTGCATTGT TTGTTATCCA
2801 AGTCAGCATC TGTCTCTGGA GCAGCATACA CAGAAATTAG AGCTCTGGTT
2851 GCAGCTAAAA GTGTTAAACT GCAAAGTTTT TTCAGCCAGT ATAAGAAACC
2901 CATCTGTCAG TTTTGGTAG AATCCCTTCA CTCTAGTCAG ATGACAGCAC
2951 TTCCGAATAC TCCATGCCAG AATGCTGACG TCGGAAAACA AGATGTGGCT
3001 CACCAGAGAG AAATGGCTTT AAATACGTTG TCTGAAATTG CCAACGTTTT
3051 CGACTTTCCT GATCTTAATC GTTTCTTAC TAGGACATTA CAAGTTCTAC
3101 TACCTGATCT TGCTGCCAAA GCAAGCCCTG CAGCTTCTGC TCTCATTCGA
3151 ACTTTAGGAA AACAATTAAA TGTCAATCGT AGAGAGATTT TAATAAACAA
3201 CTTCAAATAT ATTTTTCTC ATTTGGTCTG TTCTTGTTCC AAAGATGAAT
3251 TAGAACGTGC CCTTCATTAT CTGAAGAATG AAACAGAAAT TGAAGTGGG
3301 AGCCTGTTGA GACAAGATTT CCAAGGATTG CATAATGAAT TATTGCTGCG
3351 TATTGGAGAA CACTATCAAC AGGTTTTTAA TGGTTTGTC AACTTGCCT
3401 CATTTGCATC CAGTGATGAT CCATATCAGG GCCCAGAGA TATCATATCA
3451 CCTGAACTGA TGGCTGATTA TTTACAACCC AAATTGTTGG GCATTTTGGC
3501 TTTTTTTAAC ATGCAGTTAC TGAGCTCTAG TGTGGCATT GAAGATAAGA
3551 AAATGGCCTT GAACAGTTTG ATGTCCTTGA TGAAGTTAAT GGGACCCAAA
3601 CATGTCAGTT CTGTGAGGGT GAAGATGATG ACCACACTGA GAACTGGCCT
3651 TCGATTCAAG GATGATTTTC CTGAATTGTG TTGCAGAGCT TGGGACTGCT
3701 TTGTTGCTG CCTGGATCAT GCTTGTCTGG GCTCCCTTCT CAGTCATGTA
3751 ATAGTAGCTT TGTTACCTCT TATACACATC CAGCCTAAAG AAAGTGCAGC
3801 TATCTTCCAC TACCTCATAA TTGAAAACAG GGATGCTGTG CAAGATTTTC
3851 TTCATGAAAT ATATTTTTTA CCTGATCATC CAGAATTAAA AAAGATAAAA
3901 GCGTTTCTCC AGGAATACAG AAAGGAGACC TCTGAGAGCA CTGATCTTCA
3951 GACAACTCTT CAGCTCTCTA TGAAGGCCAT TCAACATGAA AATGTGATG
4001 TTGTTATTCA TGCTCTTACA AGCTTGAAGG AAACCTTGTA TAAAAATCAG
4051 GAAAACTGA TAAAGTATGC AACAGACAGT GAAACAGTAG AACCTATTAT
4101 CTCACAGTTG GTGACAGTGC TTTTGAAAGG TTGCCAAGAT GCAAACTCTC
4151 AAGCTGGTT GCTCTGTGGG GAATGTTTAG GGAATTGGG GCGATAGAT

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Figure 8b (iv)

4201 CCAGGTCGAT TAGATTTCTC AACAACTGAA ACTCAAGGAA AAGATTTTAC
4251 ATTTGTGACT GGAGTAGAAG ATTCAAGCTT TGCCTATGGA TTATTGATGG
4301 AGCTAACAAAG AGCTTACCTT GCGTACGCTG ATAATAGCCG AGCTCAAGAT
4351 TCAGCTGCCT ATGCCATTCA GGAGTTGCTT TCTATTTATG ACTGTAGAGA
4401 GATGGAGACC AACGGCCCAG GTCACCAATT GTGGAGGAGA TTTCCTGAGC
4451 ATGTTGGGA AATACTAGAA CCTCATCTAA ATACCAGATA CAAGAGTTCT
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4601 TTACAAAGGT TCGACATGAT CTGCCAGTA AAATTTTCAC CTGCTGTAGC
4651 ATTATGATGA AGCATGATTT CAAAGTGACC ATCTATCTTC TTCCACATAT
4701 TCTGGTGTAT GTCTTACTGG GTTGTAATCA AGAAGATCAG CAGGAGGTTT
4751 ATGCAGAAAT TATGGCAGTT CTAAAGCATG ACGATCAGCA TACCATAAAT
4801 ACCCAAGACA TTGCATCTGA TCTGTGTCAA CTCAGTACAC AGACTGTGTT
4851 CTCCATGCTT GACCATCTCA CACAGTGGGC AAGGCACAAA TTTCAGGCAC
4901 TGAAAGCTGA GAAATGTCCA CACAGCAAAT CAAACAGAAA TAAGGTAGAC
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5001 TCTAGACCTC ATACCCCAGG ATACTCTGGC AGTAGCTTCC TTTCGCTCCA
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5101 AAGCAAAATA TTCAGGAACA TCTTGGATTT TTACAGAAAT TGTATGCTGC
5151 TATGCATGAA CCTGATGGAG TGGCCGGAGT CAGTGCAATT AGAAAGGCAG
5201 AACCATCTCT AAAAGAACAG ATCCTTGAAC ATGAAAGCCT TGGCTTGCTG
5251 AGGGATGOCA CTGCTTGTTA TGACAGGGCT ATTCTAGCTAG AACCAGACCA
5301 GATCATTCAT TATCATGGTG TAGTAAAGTC CATGTTAGGT CTTGGTCAGC
5351 TGTCTACTGT TATCACTCAG GTGAATGGAG TGCATGCTAA CAGGTCCGAG
5401 TGGACAGATG AATTAAACAC GTACAGAGTG GAAGCAGCTT GGAAATTGTC
5451 ACAGTGGGAT TTGGTGGAAA ACTATTTGGC AGCAGATGGA AAATCTACAA
5501 CATGGAGTGT CAGACTGGGA CAGCTATTAT TATCAGCCAA AAAAAGAGAT
5551 ATCAGAGCTT TTTATGACTC ACTGAAACTA GTGAGAGCAG AACAAATTGT
5601 ACCTCTTTCA GCTGCAAGCT TTGAAAGAGG CTCTACCAA CGAGGATATG
5651 AATATATTGT GAGATTGCAC ATGTTATGTG AGTTGGAGCA TAGCATCAAA
5701 CCACCTTTC AGCATCTCC AGGTGACAGT TCTCAAGAAG ATTCTCTAAA
5751 CTGGGTAGCT CGACTAGAAA TGACCCAGAA TTCTACAGA GCCAAGGAGC
5801 CTATCTGGC TCTCCGGAGG GCTTTACTAA GCTCAACAA AAGACCAGAT
5851 TACAAATGAAA TGGTTGGAGA ATGCTGGCTG CAGAGTGOCA GGGTAGCTAG

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Figure 8b (v)

5901 AAAGGCTGGT CACCACCAGA CAGCCTACAA TGCTCTCCTT AATGCAGGGG
 5951 AATCACGACT CGCTGAACTG TACGTGGAAA GGGCAAAGTG GCTCTGGTCC
 6001 AAGGGTGTATG TTCACCAGGC ACTAATTGTT CTTCAAAAAG GTGTTGAATT
 6051 ATGTTTTCCT GAAAATGAAA CCCACCTGA GGGTAAGAAC ATGTTAATCC
 6101 ATGGTCGAGC TATGCTACTA GTGGGCCGAT TTATGGAAGA AACAGCTAAC
 6151 TTTGAAAGCA ATGCAATTAT GAAAAAATAT AAGGATGTGA CCGCGTGCCT
 6201 GCCAGAATGG GAGGATGGGC ATTTTACCT TGCCAAGTAC TATGACAAAT
 6251 TGATGCCCAT GGTACAGAC AACAAAATGG AAAAGCAAGG TGATCTCATC
 6301 CGGTATATAG TTCTTCATTT TGGCAGATCT CTACAATATG GAAATCAGTT
 6351 CATATATCAG TCAATGCCAC GAATGTTAAC TCTATGGCTT GATTATGGTA
 6401 CAAAGGCATA TGAATGGGAA AAAGCIGGCC GCTCCGATCG TGTACAAATG
 6451 AGGAATGATT TGGGTAAAAT AAACAAGGTT ATCACAGAGC ATACAAACTA
 6501 TTTAGCTCCA TATCAATTTT TGA CTGCTTTT TTCACAATTG ATCTCTCGAA
 6551 TTTGTCAATC TCACGATGAA GTTTTGTGTG TCTTGATGGA AATAATAGCC
 6601 AAAGTATTTT TAGCCTATCC TCAACAAGCA ATGTGGATGA TGACAGCTGT
 6651 GTCAAAGTCA TCTTATCCCA TGCGTGTGAA CAGATGCAAG GAAATCCTCA
 6701 ATAAAGCTAT TCATATGAAA AAATCCTTAG AGAAGTTTGT TGGAGATGCA
 6751 ACTCGCCTAA CAGATAAGCT TCTAGAATTG TGCAATAAAC CGGTTGATGG
 6801 AAGTAGTTCC ACATTAAGCA TGAGCACTCA TTTTAAAATG CTTAAAAAGC
 6851 TGGTAGAAGA AGCAACATTT AGTGAAATCC TCATTCTCTT ACAATCAGTC
 6901 ATGATACCTA CACTTCCATC AATTCTGGGT ACCCATGCTA ACCATGCTAG
 6951 CCATGAACCA TTCTCTGGAC ATTGGGCCTA TATTGCAGGG TTTGATGATA
 7001 TGGTGGAAAT TCTTGCTTCT CTTCAGAAAC CAAAGAAGAT TTCTTTAAAA
 7051 GGCTCAGATG GAAAGTTCTA CATCATGATG TGTAAGCCAA AAGATGACCT
 7101 GAGAAAGGAT TGTAAGCTAA TGGAATTCAA TTCCTTGATT AATAAGTGCT
 7151 TAAGAAAAGA TGCAGAGTCT CGTAGAAGAG AACTTCATAT TCGAACATAT
 7201 GCAGTTATTC CACTAAATGA TGAATGTGGG ATTATTGAAT GGGTGAACAA
 7251 CACTGCTGGT TTGAGACCTA TTCTGACCAA ACTATATAAA GAAAAGGGAG
 7301 TGTATATGAC AGGAAAAGAA CTTGCGCAGT GTATGCTACC AAAGTCAGCA
 7351 GCTTTATCTG AAAAATCAA AGTATTCCGA GAATTTCTCC TGCCAGGCA
 7401 TCCTCCTATT TTTCATGAGT GGTTCCTGAG AACATTCCCT GATCCTACAT
 7451 CATGGTACAG TAGTAGATCA GCTTACTGCC GTTCCACTGC AGTAATGTCA
 7501 ATGGTTGGTT ATATTCTGGG GCTTGGAGAC CGTCATGGTG AAAATATTCT

Figure 8b (v1)

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7551 CTTTGATTCT TTGACTGGTG AATGCGTACA TGTAGATTTC AATTGTCTTT
7601 TCAATAAGGG AGAAACCTTT GAAGTTCCAG AAATTGTGCC ATTTCCGCTG
7651 ACTCATAATA TGGTTAATGG AATGGGTCCT ATGGGAACAG AGGGTCTTTT
7701 TCGAAGAGCA TGTGAAGTTA CAATGAGGCT GATGCGTGAT CAGCGAGAGC
7751 CTTTAATGAG TGTCTTAAAG ACTTTCCTAC ATGATCCTCT TGTGGAATGG
7801 AGTAAACCAG TGAAAGGGCA TTCCAAAGCG CCACTGAATG AAAGTGGAGA
7851 AGTTGTCAAT GAAAAGGCCA AGACCCATGT TCTTGACATT GAGCAGCGAC
7901 TACAAGGTGT AATCAAGACT CGAAATAGAG TGACAGGACT GCCGTATCT
7951 ATTGAAGGAC ATGTGCATTA CCTTATACAG GAAGCTACTG ATGAAAACCT
8001 ACTATGCCAG ATGTATCTTG GTTGGACTCC ATATATGTGA AATGAAATTA
8051 TGTAAGAGAA TATGTTAATA ATCTAAAAGT AATGCATTTG GTATGAATCT
8101 GTGGTTGTAT CTGTTCAATT CTAAAGTACA ACATAAATTT ACGTTCCTCAG
8151 CAACTGTTAT TTCTCTCTGA TCATTAATTA TATGTAAAAT AATATACATT
8201 CACTCGTGCC
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Figure 9a (1)

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!!NA_SEQUENCE 1.0
ID   HS349941   standard; RNA; HUM; 12780 BP.
XX
AC   U34994;
XX
NI   g995940
XX
DT   26-SEP-1995 (Rel. 45, Created)
DT   22-FEB-1997 (Rel. 51, Last updated, Version 4)
XX
DE   Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs)
DE   mRNA, complete cds.
XX
KW   .
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-12780
RX   MEDLINE; 95401275.
RA   Hartley K.O., Gell D., Smith G.C., Zhang H., Divecha N., Connelly M.A.,
RA   Admon A., Lees-Miller S.P., Anderson C.W., Jackson S.P.;
→ RT   "DNA-dependent protein kinase catalytic subunit: a relative of
RT   phosphatidylinositol 3-kinase and the ataxia telangiectasia gene
RT   product";
RL   Cell 82:849-856(1995).
XX
RN   [2]
RP   1-12780
RA   Gell D.;
RT   ;
RL   Submitted (29-AUG-1995) to the EMBL/GenBank/DDBJ databases.
RL   Dave Gell, Zoology, Wellcome/CRC, Tennis Court Road, Cambridge CB2 1QR,
RL   UK
XX
DR   SPTREMBL; Q13327; Q13327.
XX
CC   NCBI gi: 995940
XX
FH   Key          Location/Qualifiers
FH
FT   source          1. .12780
FT                   /organism="Homo sapiens"
FT                   /chromosome="8"
FT                   /cell_type="He-La"
FT                   /map="8q11"
FT   CDS             53. .12343
FT                   /codon_start=1
FT                   /db_xref="PID:g995941"
FT                   /db_xref="SPTREMBL:Q13327"
FT                   /note="DNA-activated protein kinase catalytic subunit; PI
FT                   kinase family member; partial genomic sequence located in
FT                   GenBank Accession Number L27425; Method: conceptual
FT                   translation supplied by author. NCBI gi: 995941"
FT                   /gene="DNA-PKcs"
FT                   /product="DNA dependent protein kinase catalytic subunit"
FT                   /translation="MAGSGAGVRCSSLRLQETLSAADRCGAALAGHQLIRGLGQECVLS
FT                   SSPAVLALQTSLVFSRDFGLLVFVRKSLNSIEFRECREEILKFLCIFLEKMGQKIAPYS
FT                   VEIKNTCTSVYTKDRAAKCKIPALDLLIKLLQTFRSSRLMDEFKIGELFSKFYGELALK
FT                   KKIPDTVLEKVVYELLGGLGEVHPSEMINNAENLFRAFLGELKTQMTSAVREPKLPLVLAG
FT                   CLKGLSSLLCNFTKSMEEDPQTSREIFNFVLKAIRPQIDLKRYAVPSAGLRLFALHASQ
FT                   FSTCLLDNYVSLFEVLLKWCAGHTNVELKKAALSALESFLKQVSNMVAKNAEMHKNKLOY
FT                   FMEQFYGIIRNVDSNNKELSLAIRGYGLFAGPCKVINAKDVDFMYVELIQRCCKQMFLLTQ
FT                   TDTGDIRVYQMPFSLQSVASVLLYLDTVPEVYTFVLEHLVVMQIDSFQYSPKMQLVCC
FT                   RAIVKVFLAALAKGPVLRNCISTVVHQGLIRICSKPVVLPKGPESSESDHRASGEVRTG

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Figure 9 (ii)

FT KWKVPTYKDYVDLFRHLLSSDQMDSILADEAFFSVNSSSESLNHLLYDEFVKSVLKIV
 FT EKLDLTLEIQTVGEQENGDEAPGVWMIPTSDPAANLHPAKPKDFSANLVEFCREILP
 FT EKQAEFFEPWVYSFSYELILQSTRPLISGFYKLLSITVRNAKKIKYFEGVSPKSLKHS
 FT PEDPEKYSCFALFVKFGKEVAVKMKQYKDELLASCLTFLLSLPHNIIELDVRAYVPALQ
 FT MAFKLGLSYTPLAEVGLNAALEEWSIYIDRHVMQPYKIDILPCLDGYLKTALSDETQNN
 FT WEVSALSRAAQKGFNVVLKHLKKTKNLSSNEAISLEEIRIRVVQMLGSLGGQINKNLL
 FT TVTSSDEMKSYSVAWDREKRLSFAVPPREMKPVI FLDVFLPRVTELALTASDRQTKVAA
 FT CELLHSMVMFMLGKATQMPGEGGQAPPMYQLYKRTFPVLLRLACDQVTRQLYEPLVM
 FT QLIHWFTNNKKFESQDTVSLLEAILDGI VDPVDSTLRDFCGRCIREFLKWSIKQITPQQ
 FT QEKSPVNTKSLFKRLYSLALHPNAFKRLGASLAFNNIYREFREEESLVEQFVFEALVTY
 FT MESLALAHADEKSLGTIOCCDAIDHLCRI IEKKHVS LNKA KRRRLPRGFPPSASLCLL
 FT DLVKWLLAHCGRPQTECRHKSIELFYKFVPLLPGNRSPNLWLKDVLEEGVSFLINTFE
 FT GGGCGQPSGILAQPTLLYLGRPFSLQATLCWLDLLAALCEYNTFIGERTVGALQVLGT
 FT EAQSSLLKAVAFFLESIAMHDI IAAEKCFGTGAAGNRTSPQEGERYNSKCTVVVRIME
 FT FTTTLNTPSGWMLKDLKDLNTHLMRVLVQTLCEPASIGFNIGDVQVMAHLPDVCVNL
 FT MKALKMSPYKIDILETHLREKITAQSIEELCAVNLYGPDAQVDRSRLAAVVSACKQLHRA
 FT GLLHNILPSQSTDLHHSVGTTELLSLVYKGIAPGDERQCLPSLDLSCKQLASGLLELFAFA
 FT FGGLCERLVSLLLNPAVLSTASLGSSQGSVHFSHGEYFYSLSFSETINTELLKNLDAV
 FT LELMQSSVDNTKMSAVLNGMLDQSFREANQKHQGLKLATTILQHKKCDSWWAKDSP
 FT LETKMAVLALLAKILQIDSSVSFNTSHGSFPEVFTTYISLLADTKLDLHKGQAVTLLP
 FT FFTSLTGGSLLELRRVLEQLIVAHFPMOSREFPEGTFRFNMYVDCMKKFLDALELSQSP
 FT MLLELMTVELCREQQHVMELFQSSFRRIARRGSCVTQVGLLESVYEMFRKDDPRLSFT
 FT RQSFVDRSLTLLWHCSLDALREFSTIVVDAIDVLKSRFTKLNSTFDTQITKMGYY
 FT KILDVMSRLPKDDVHAKESKINQVFGSCITEGNETKTLLIKLCYDAHNLNAGENQL
 FT LERRRLYHCAAYNCAISVICCVNELKFYQGFLFSEKPEKNLLIFENIDLKRRYNFPV
 FT EVEVPMERKKKYIEIRKEAREAAANGSDGPSYMSLSYLADSTLSEEMSQFDFSTGVQS
 FT YSYSSQDPRPATGRFRREQRDPTVHDDVLELEMDENRHECMAPLTALVKHMHRSGLP
 FT PQGEEDSVPRDLPDPSWMKFLHGKLGNPVPLNIRLFLAKLVINTEEVFRPYAKHWSLPL
 FT QLAASENNGGEGIHVMVEIVATILSWTGLATPTGVPKDEVLANRLNLFMLKHVHFHPR
 FT AVFRHNLEI IKTLVECKWDCLSIPYRLIFEKFSGKDPNSKDNVSGIQLLGIVMANDLPP
 FT YDPQCGIQSSEYFQALVNMSFVRYKEVYAAAAEVLGLILRYVMERNILEESLCELVA
 FT KQLKQHONTMEDKIVCLNKVTKSFPLADRFMNAVFFLLPKFHVGLRLNLCLEVLCRV
 FT EGMTLEYFOLKSKDFVQVMRHRDERQKVCLDIIYKMPKLPVELRELNPVVEFVSHP
 FT STTCREQMYNIMLWIHDNYRDPESSETDNDSEIFKLAQDLIQGLIDENPGLQIIRNF
 FT WSHETRLPSNTLDRLLALNSLYSPKIEVHFLSLATNLFLEMTSMSPDPYPMFHEPLSE
 FT CEFOEYTDIDSDWRSTVLTPMFVETQASQGLTQTRTQEGSLSARWPVAGQIRATQQQH
 FT DFTLTQTADGRSSFDWLTGSSSTDPLVDHTSPSSDLSLFAHKSERLQRAPLKSVPDFG
 FT KKRLGLPGDEVNDKVKGAAGRTDLLRLRRRFMRDQEKLSLMYARKGVAEQKREKEIKSE
 FT LKMKQDAQVVLRSYRHGDLDPDIQIKHSSLITPLQAVAQRPDI IAKQLFSSLSFGILKE
 FT MDKFKTLSEKNNTQKLLQDENRFLNTTFSFFPPFVSCIQDISCOHAALLSLDPAVSA
 FT GCLASLQOPVGIRLLEALRLPLPAELPAKRVRGKARLPDVLRLWVELAKLYRSIGEYD
 FT VLRGIFTSEIGTKQITQSALLAEARSDYSEAAKQYDEALNKQDWVDGEPTAEKDFWEL
 FT ASLDCYNHLAEWKSLEYCSTASIDSENPPDLNKIWSEPFYQETYLPMIRSKLKLLOG
 FT EADQSLTTFIDKAMHGELOKAILLEHYSQELSLLYLLQDDVDRAKYIIONGQSFQNY
 FT SSIDVLLHQSRITKLQSVQALTEIQEFISFISKQGNLSSQVPLKRLNLTWINRYPDAM
 FT DPMNIWDDIITNRCFFLSKIEEKLTPPEDNSMNVDDQDPSDRMEVQEQEEDISSLR
 FT SCKFSMKMKMIDSARKQNNFSLAMKLLKELHKESTTRDVLVSWVQSYCRLSHCRSRSQ
 FT GCSEQVLTVLKTVSLDENNVSSYLXKNILAFRDQNTILGTTTIRI IANALSSEPACLAE
 FT IEEDKARRILELSSGSSSEDESKVIAGLYQRAFOHLSEAVQAAEEEAQPPSWCGPAAGV
 FT IDAYMTLADFCDQQLRKEENASVTDSAELQAYPALVVEKMLKALKLNSNEARLKFPRL
 FT LQIIERYPEETLSLMTKEISSVPCWQFISWISHMVALLDKDAQAVAVQHSVEEITINYPQ
 FT AIVYFFIISSESYFSDTSTGHKNKEFVARIKSKLDQGGVIQDFINALDQLSNPPELLFK
 FT DWSNDVRAELAKTPVNKKNIEKMYERMYAALGDPKAPGLGAFRRKFIQTFGKEFDKHF
 FT KGGSKLLRMKLSDFNDITNMLLLKMNKDSKPPGNLKECSPWMSDFKVEFLRNELEIPGQ
 FT YDGRGKPLPEYHVRIAGFDERVTVMASLRPKRIIRGHDEREHPFLVKGEDLRQDQR
 FT VBQLFQVMNGILAQDSACSQRALQLRTYSVVPMTSSDPRAPCEYKDWLTKMSGKHIDV
 FT AYMLMYKGANRTETVTSFRKRESKVPADLLKRAFRMSTSPFAFLALRSHFASHALIC
 FT ISHWILGIGDRHLNFMVAMETGGVIGIDFGHAFGSATQFLPVPPELMPFRLTRQFINLM
 FT LPMKETGLMYSIMVHALRAFRSDPGLLTNTMDVVFKEPSFDWKNFEQKMLKGGSWIQE
 FT INVAEKWYPRQKICYAKRKLAPANPAVITCDELLLGHEKAPAFRDYVAVARGSKDHNI
 FT RAQEPESGLSEETQVKCLMDQATDPNLTGRTWEGWEPWM*
 XX
 SQ Sequence 12780 BP; 3612 A; 2769 C; 3084 G; 3314 T; 1 other;

U34994 Length: 12780 July 10, 1998 12:15 Type: N Check: 8189 .. Figure 9b(1)

1 ATTTCCGGGT CCGGGCCGAG CGGGCGCAG CGGGGAGCG GGACTCGGCG

Figure 9b (ii)

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101 GAGACCTTGT CCGCTGCGGA CCGCTGCGGT GCTGCCCTGG CCGGTCATCA
151 ACTGATCCGC GGCCTGGGGC AGGAATGCGT CCTGAGCAGC AGCCCGCGG
201 TGCTGGCATT ACAGACATCT TTAGTTTTTT CCAGAGATTT CGGTTTGCTT
251 GTATTTGTCC GGAAGTCACT CAACAGTATT GAATTTCTGT AATGTAGAGA
301 AGAAATCCTA AAGTTTTTAT GTATTTTCTT AGAAAAATG GGCCAGAAGA
351 TCGCACCTTA CTCTGTTGAA ATTAAGAACA CTTGTACCAG TGTTTATACA
401 AAAGATAGAG CTGCTAAATG TAAAAATCCA GCCCTGGACC TTCTTATTAA
451 GTTACTTCAG ACTTTTAGAA GTTCTAGACT CATGGATGAA TTTAAAATTG
501 GAGAATTATT TAGTAAATTC TATGGAGAAC TTGCATTGAA AAAAAAATA
551 CCAGATACAG TTTTAGAAAA AGTATATGAG CTCCTAGGAT TATTGGGTGA
601 AGTTCATCCT AGTGAGATGA TAAATAATGC AGAAAACTG TTCCGCGCTT
651 TTCTGGGTGA ACTTAAGACC CAGATGACAT CAGCAGTAAG AGAGCCCAA
701 CTACCTGTTT TGGCAGGATG TCTGAAGGGG TTGTCCTCAC TTCTGTGCAA
751 CTTCACTAAG TCCATGGAAG AAGATCCCCA GACTTCAAGG GAGATTTTTA
801 ATTTTGTACT AAAGGCAATT CGTCTCAGA TTGATCTGAA GAGATATGCT
851 GTGCCCTCAG CTGGCTTGCG CCTATTTGCC CTGCATGCAT CTCAGTTTAG
901 CACCTGCCTT CTGGACAAC ACGTGTCTCT ATTTGAAGTC TTGTTAAAGT
951 GGTGTGCCCA CACAAATGTA GAATTGAAAA AAGCTGCACT TTCAGCCCTG
1001 GAATCCTTTC TGAAACAGGT TTCTAATATG GTGGCGAAAA ATGCAGAAAT
1051 GCATAAAAAAT AAAGTGCAGT ACTTTATGGA GCAGTTTTAT GGAATCATCA
1101 GAAATGTGGA TTCGAACAAC AAGGAGTTAT CTATTGCTAT CCGTGGATAT
1151 GGACTTTTTG CAGGACCGTG CAAGGTTATA AACGCAAAAG ATGTTGACTT
1201 CATGTACGTT GAGCTCATT AGCGCTGCAA GCAGATGTTT CTCACCCAGA
1251 CAGACACTGG TGACTACCGT GTTTATCAGA TGCCAAGCTT CCTCCAGTCT
1301 GTTGCAAGCG TCTTGCTGTA CCTTGACACA GTTCCTGAGG TGTATACTCC
1351 AGTTCTGGAG CACCTCGTGG TGATGCAGAT AGACAGTTTC CCACAGTACA
1401 GTCCAAAAAT GCAGCTGGTG TGTGTCAGAG CCATAGTGAA GGTGTTCTTA
1451 GCTTTGGCAG CAAAAGGGCC AGTTCTCAGG AATTGCATTA GTACTGTGGT
1501 GCATCAGGGT TTAATCAGAA TATGTTCTAA ACCAGTGGTC CTTCCAAAGG
1551 GCCCTGAGTC TGAATCTGAA GACCACCGTG CTTCAGGGGA AGTCAGAACT
1601 GGCAAATGGA AGGTGCCCAC ATACAAAGAC TACGTGGATC TCTTCAGACA
1651 TCTCCTGAGC TCTGACCAGA TGATGGATT CTTTTAGCA GATGAAGCAT

Figure 9b (111)

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1701 TTTTCTCTGT GAATTCCTCC AGTGAAAGTC TGAATCATTT ACTTTATGAT
1751 GAATTTGTAA AATCCGTTTT GAAGATTGTT GAGAAATTGG ATCTTACACT
1801 TGAAATACAG ACTGTTGGGG AACAAAGAGAA TGGAGATGAG GCGCCTGGTG
1851 TTTGGATGAT CCCAACTTCA GATCCAGCGG CTAACCTGCA TCCAGCTAAA
1901 CCTAAAGATT TTTGCGCTTT CATTAACCTG GTGGAATTTT GCAGAGAGAT
1951 TCTCCCTGAG AAACAAGCAG AATTTTTTTGA ACCATGGGTG TACTCATTTT
2001 CATATGAATT AATTTTGTAA TCTACAAGGT TGCCCTCAT CAGTGGTTTC
2051 TACAAATTGC TTTCTATTAC AGTAAGAAAT GCCAAGAAAA TAAAATATTT
2101 CGAGGGAGTT AGTCCAAAGA GTCTGAAACA CTCTCCTGAA GACCCAGAAA
2151 AGTATTCTTG CTTTGCTTTA TTTGTGAAAT TTGGCAAAGA GGTGGCAGTT
2201 AAAATGAAGC AGTACAAAGA TGAACCTTTTG GCCTCTTGTT TGACCTTTCT
2251 TCTGTCCTTG CCACACAACA TCATTGAACT CGATGTTAGA GCCTACGTTT
2301 CTGCACTGCA GATGGCTTTC AAACCTGGCC TGAGCTATAC CCCCTTGGCA
2351 GAAGTAGGCC TGAATGCTCT AGAAGAATGG TCAATTTATA TTGACAGACA
2401 TGTAATGCAG CCTTATTACA AAGACATTCT CCCCTGCCTG GATGGATACC
2451 TGAAGACTTC AGCCTTGTC AATGAGACCA AGAATAACTG GGAAGTGTC A
2501 GCTCTTTCTC GGGCTGCCA GAAAGGATTT AATAAAGTGG TGTAAAGCA
2551 TCTGAAGAAG ACAAGAACC TTTTATCAAA CGAAGCAATA TCCTTAGAAG
2601 AAATAAGAAT TAGAGTAGTA CAAATGCTTG GATCTCTAGG AGGACAAATA
2651 AACAAAAATC TTCTGACAGT CACGTCCTCA GATGAGATGA TGAAGAGCTA
2701 TGTGGCCTGG GACAGAGAGA AGCGGCTGAG CTTTGCACTG CCCTTTAGAG
2751 AGATGAAACC TGTCAATTTT CTGGATGTGT TCCTGCCTCG AGTCACAGAA
2801 TTAGCGCTCA CAGCCAGTGA CAGACAACT AAAGTTGCAG CCTGTGAACT
2851 TTTACATAGC ATGGTTATGT TTATGTTGGG CAAAGCCACG CAGATGCCAG
2901 AAGGGGGACA GGGAGCCCCA CCCATGTACC AGCTCTATAA GCGGACGTTT
2951 CCTGTGCTGC TTOGACTTGC GTGTGATGTT GATCAGGTGA CAAGGCAACT
3001 GTATGAGCCA CTAGTTATGC AGCTGATTCA CTGGTTCACT AACACAAGA
3051 AATTTGAAAG TCAGGATACT GTTCTCTTAC TAGAAGCTAT ATTGGATGGA
3101 ATTGTGGACC CTGTTGACAG TACTTTAAGA GATTTTTGTG GTGGGTGTAT
3151 TCGAGAATTC CTTAAATGGT CCATTAAGCA AATAACACCA CAGCAGCAGG
3201 AGAAGAGTCC AGTAAACACC AAATCGCTTT TCAAGCGACT TTATAGCCTT
3251 GCGCTTCACC CCAATGCTTT CAAGAGGCTG GGAGCATCAC TTGCCTTTAA
3301 TAATATCTAC AGGGAATTCA GGAAGAAGA GTCTCTGGTG GAACAGTTTG
3351 TGTTTGAAGC CTTGGTGATA TACATGGAGA GTCTGGCCTT AGCACATGCA

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Figure 9b (iv)

3401 GATGAGAAGT CCTTAGGTAC AATTCAACAG TGTGTGATG CCATTGATCA
3451 CCTATGCCGC ATCATTGAAA AGAAGCATGT TTCTTTAAAT AAAGCAAAGA
3501 AACGACGTTT GCCGCGAGGA TTTCACCTT CCGCATCATT GTGTTTATTG
3551 GATCTGGTCA AGTGGCTTTT AGCTCATTTGT GGGAGGCCCC AGACAGAATG
3601 TCGACACAAA TCCATTGAAC TCTTTTATAA ATTCGTTTCTT TTATTGCCAG
3651 GCAACAGATC CCCTAATTGT TGGCTGAAAG ATGTTCTCAA GGAAGAAGGT
3701 GTCTCTTTTC TCATCAACAC CTTTGAGGGG GGTGGCTGTG GCCAGCCCTC
3751 GGGCATCCTG GCCCAGCCCA CCCTCTTGTA CCTTCGGGGG CCATTGAGCC
3801 TGCAGGCCAC GCTATGCTGG CTGGACCTGC TCCTGGCCGC GTTGGAGTGC
3851 TACAACACGT TCATTGGCGA GAGAACTGTA GGAGCGCTCC AGGTCCTAGG
3901 TACTGAAGCC CAGTCTTCAC TTTTGAAAGC AGTGGCTTTC TTCTTAGAAA
3951 GCATTGCCAT GCATGACATT ATAGCAGCAG AAAAGTGCTT TGGCACTGGG
4001 GCAGCAGGTA ACAGAACAAG CCCACAAGAG GGAGAAAGGT ACAACTACAG
4051 CAAATGCACC GTTGTGGTCC GGATTATGGA GTTTACCACG ACTCTGCTAA
4101 ACACCTCCCC GGAAGGATGG AAGCTCCTGA AGAAGGACTT GTGTAATACA
4151 CACCTGATGA GAGTCCTGGT GCAGACGCTG TGTGAGCCCG CAAGCATAGG
4201 TTTCAACATC GGAGACGTCC AGGTTATGGC TCATCTTCCT GATGTTTGTG
4251 TGAATCTGAT GAAAGCTCTA AAGATGTCCC CATACAAAGA TATCCTAGAG
4301 ACCCATCTGA GAGAGAAAAT AACAGCACAG AGCATTGAGG AGCTTTGTGC
4351 CGTCAACTTG TATGGCCCTG ACGCGCAAGT GGACAGGAGC AGGCTGGCTG
4401 CTGTTGTGTC TGCCGTGAAA CAGCTTCACA GAGCTGGGCT TCTGCATAAT
4451 ATATTACCGT CTCAGTCCAC AGATTTGCAT CATTCTGTTG GCACAGAACT
4501 TCTTTCCCTG GTTTATAAAG GCATTGCCCC TGGAGATGAG AGACAGTGTC
4551 TGCCTTCTCT AGACCTCAGT TGTAAGCAGC TGGCCAGCGG ACTTCTGGAG
4601 TTAGCCTTTG CTTTGGAGG ACTGTGTGAG CGCCTTGTA GTCTCTCTCT
4651 GAACCCAGCG GTGCTGTCCA CGGCGTCTT GGGCAGCTCA CAGGGCAGCG
4701 TCATCCACTT CTCCCATGGG GAGTATTTCT ATAGCTTGTT CTCAGAAACG
4751 ATCAACACGG AATTATTGAA AAATCTGGAT CTGCTGTAT TGGAGCTCAT
4801 GCAGTCTTCA GTGGATAATA CCAAAATGGT GAGTGCCGTT TTGAACGGCA
4851 TGTTAGACCA GAGCTTCAGG GAGCGAGCAA ACCAGAAACA CCAAGGACTG
4901 AAACCTGCGA CTACAATTCT GCAACACTGG AAGAAGTGTG ATTCATGGTG
4951 GGCCAAAGAT TCCCTCTCG AAATAAAAT GGCAGTGCTG GCCTTACTGG
5001 CAAAAATTTT ACAGATTGAT TCATCTGTAT CTTTAAATAC AAGTCATGGT

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Figure 9b (v)

5051 TCATTCCTG AAGTCTTTAC AACATATATT AGTCTACTTG CTGACACAAA
5101 GCTGGATCTA CATTTAAGG GCCAAGCTGT CACTCTTCTT CCATTCTTCA
5151 CCAGCCTCAC TGGAGGCAGT CTGGAGGAAC TTAGACGTGT TCTGGAGCAG
5201 CTCATCGTTG CTCACTTCCC CATGCAGTCC AGGGAATTTT CTCCAGGAA
5251 TCCGCGGTTT AATAATTATG TGGACTGCAT GAAAAAGTTT CTAGATGCAT
5301 TGGAATTATC TCAAAGCCCT ATGTTGTTGG AATTGATGAC AGAAGTTCTT
5351 TGTGCGGAAC AGCAGCATGT CATGGAAGAA TTATTTCAAT CCAGTTTCAG
5401 GAGGATTGCC AGAAGGGGTT CATGTGTCAC ACAAGTAGGC CTTCTGGAAA
5451 GCGTGATGA AATGTTTCAAG AAGGATGACC CCCGCCTAAG TTTACACGC
5501 CAGTCCTTTG TGGACCGCTC CCTCCTCACT CTGCTGTGGC ACTGTAGCCT
5551 GGATGCTTTG AGAGAATTCT TCAGCACAAT TGTGGTGGAT GCCATTGATG
5601 TGTGAAGTC CAGGTTTACA AAGCTAAATG AATCTACCTT TGATACTCAA
5651 ATCACCAAGA AGATGGGCTA CTATAAGATT CTAGACGTGA TGTATTCTCG
5701 CCTTCCCAA GATGATGTTT ATGCTAAGGA ATCAAAAATT AATCAAGTTT
5751 TCCATGGCTC GTGTATTACA GAAGGAAATG AACTTACAAA GACATTGATT
5801 AAATTGTGCT ACGATGCATT TACAGAGAAC ATGGCAGGAG AGAATCAGCT
5851 GCTGGAGAGG AGAAGACTTT ACCATTGTGC AGCATACAAC TGCGCCATAT
5901 CTGTCACTG CTGTGTCTTC AATGAGTTAA AATTTTACCA AGGTTTTCTG
5951 TTTAGTGAAA AACCAGAAAA GAAGTTGCTT ATTTTGTAAA ATCTGATCGA
6001 CCTGAAGCGC CGCTATAATT TTCTGTAGA AGTTGAGGTT CCTATGGAAA
6051 GAAAGAAAA GTACATTGAA ATTAGGAAAG AAGCCAGAGA AGCAGCAAAT
6101 GGGGATTGAG ATGGTCTTTC CTATATGTCT TCCCTGTCTAT ATTTGGCAGA
6151 CAGTACCTTG AGTGAGGAAA TGAGTCAATT TGATTTCTCA ACCGGAGTTC
6201 AGAGCTATTC ATACAGCTCC CAAGACCCTA GACCTGCCAC TGGTCGTTTT
6251 CGGAGACGGG AGCAGCGGGA CCCCACGGTG CATGATGATG TGCTGGAGCT
6301 GGAGATGGAC GAGCTCAATC GGCATGAGTG CATGGCGGCC CTGACGGGCC
6351 TGGTCAAGCA CATGCACAGA AGCCTGGGCC CGCCTCAAGG AGAAGAGGAT
6401 TCAGTGCCAA GAGATCTTCC TTCTTGATG AAATTCCTCC ATGGCAAAT
6451 GGGAAATCCA ATAGTACCAT TAAATATCCG TCTCTTCTTA GCCAAGCTTG
6501 TTATTAATAC AGAAGAGGTC TTTCGCCCTT ACGCGAAGCA CTGGCTTAGC
6551 CCCTTGCTGC AGCTGGCTGC TTCTGAAAC AATGGAGGAG AAGGAATTCA
6601 CTACATGGTG GTTGAGATAG TGGCCACTAT TCTTTTCATG ACAGGCTTGG
6651 CCACTCCAAC AGGGGTCCCT AAAGATGAAG TGTAGCAAA TCGATTGCTT
6701 AATTTCTTAA TGAAACATGT CTTTCATCCA AAAAGAGCTG TGTTTAGACA

Figure 9b (vi)

6751 CAACCTTGAA ATTATAAAGA CCCTTGTCGA GTGCTGGAAG GATTGTTTAT
6801 CCATCCCTTA TAGGTTAATA TTTGAAAAGT TTTCCGGTAA AGATCCTAAT
6851 TCTAAAGACA ACTCAGTAGG GATTCAATTG CTAGGCATCG TGATGGCCAA
6901 TGACCTGCCT CCCTATGACC CACAGTGTGG CATCCAGAGT AGCGAATACT
6951 TCCAGGCTTT GGTGAATAAT ATGTCCTTTG TAAGATATAA AGAAGTGTAT
7001 GCCGCTGCAG CAGAAGTTCT AGGACTTATA CTTCGATATG TTATGGAGAG
7051 AAAAAACATA CTGGAGGAGT CTCTGTGTGA ACTGGTTGCG AAACAATTGA
7101 AGCAACATCA GAATACTATG GAGGACAAGT TTATTGTGTG CTTGAACAAA
7151 GTGACCAAGA GCTTCCCTCC TCTTGCAGAC AGGTTTCATGA ATGCTGTGTT
7201 CTCTCTGCTG CCAAAATTTC ATGGAGTGTT GAAAACACTC TGTCTGGAGG
7251 TGGTACTTTG TCGTGTGGAG GGAATGACAG AGCTGTACTT CCAGTTAAAG
7301 AGCAAGGACT TCGTTCAAGT CATGAGACAT AGAGATGAAA GACAAAAAGT
7351 ATGTTTGGAC ATAATTTATA AGATGATGCC AAAGTTAAAA CCAGTAGAAC
7401 TCCGAGAACT TCTGAACCCC GTTGTGGAAT TCGTTTCCCA TCCTTCTACA
7451 ACATGTAGGG AACAAATGTA TAATATTCTC ATGTGGATTG ATGATAATTA
7501 CAGAGATCCA GAAAGTGAGA CAGATAATGA CTCCCAGGAA ATATTTAAGT
7551 TGGCAAAAGA TGTGCTGATT CAAGGATTGA TCGATGAGAA CCCTGGACTT
7601 CAATTAATTA TTCGAAATTT CTGGAGCCAT GAAACTAGGT TACCTTCAAA
7651 TACCTTGGAC CGGTGCTGG CACTAAATTC CTTATATTCT CCTAAGATAG
7701 AAGTGCAC TTAAAGTTTA GCAACAAATT TTCTGCTCGA AATGACCAGC
7751 ATGAGCCCAG ATTATCCAAA CCCCATGTTT GAGCATCCTC TGTGAGAATG
7801 CGAATTTTCA GAATATACCA TTGATTCTGA TTGGCGTTTC CGAAGTACTG
7851 TTCTCACTCC GATGTTTGTG GAGACCCAGG CCTCCCAGGG CACTCTCCAG
7901 ACCCGTACCC AGGAAGGGTC CCTCTCAGCT CGCTGGCCAG TGGCAGGGCA
7951 GATAAGGGCC ACCCAGCAGC AGCATGACTT CACTGACA CAGACTGCAG
8001 ATGGAAGAAG CTCATTTGAT TGGCTGACCG GGAGCAGCAC TGACCCGCTG
8051 GTCGACCACA CCAGTCCCTC ATCTGACTCC TTGCTGTTTG CCCACAAGAG
8101 GAGTGAAAGG TTACAGAGAG CACCCTTGAA GTCAGTGGGG CCTGATTTTG
8151 GGAAAAAAG GCTGGGCCTT CCAGGGGACG AGGTGGATAA CAAAGTGAAA
8201 GGTGCGGCCG GCCGGACGGA CCTACTACGA CTGCGCAGAC GGTTTATGAG
8251 GGACCAGGAG AAGCTCAGTT TGATGTATGC CAGAAAAGGC GTTGTCTGAGC
8301 AAAAAACAGA GAAGGAAATC AAGAGTGAGT TAAAAATGAA GCAGGATGCC
8351 CAGGTGTTT TGTACAGAAG CTACCGGCAC GGAGACCTTC CTGACATTCA

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Figure 9b (v11)

8401 GATCAAGCAC AGCAGCCTCA TCACCCCGTT ACAGGCCGTG GCCCAGAGGG
 8451 ACCCAATAAT TGCAAAACAG CTCTTTAGCA GCTTGTTTTTC TGGAATTTTG
 8501 AAAGAGATGG ATAAATTTAA GACACTGTCT GAAAAAACA ACATCACTCA
 8551 AAAGTTGCTT CAAGACTTCA ATCGTTTTCT TAATACCACC TTCTCTTTCT
 8601 TTCCACCCCTT TGTCTCTTGT ATTGAGGACA TTAGCTGTCA GCACGCAGCC
 8651 CTGCTGAGCC TCGACCCAGC GGCTGTTAGC GCTGGTTGCC TGGCCAGCCT
 8701 ACAGCAGCCC GTGGGCATCC GCCTGCTAGA GGAGGCTCTG CTCCGCCTGC
 8751 TGCCTGCTGA GCTGCCTGCC AAGCGAGTCC GTGGGAAGGC CCGCCTCCCT
 8801 CCTGATGTCC TCAGATGGGT GGAGCTTGCT AAGCTGTATA GATCAATTGG
 8851 AGAATACGAC GTCCTCCGTG GGATTTTTAC CAGTGAGATA GGAACAAAGC
 8901 AAATCACTCA GAGTGCATTA TTAGCAGAAG CCAGAAGTGA TTATTTCTGAA
 8951 GCTGCTAAGC AGTATGATGA GGCTCTCAAT AAACAAGACT GGGTAGATGG
 9001 TGAGCCCA CA GAAGCCGAGA AGGATTTTTG GGAAGTTGCA TCCCTTGACT
 9051 GTTACAACCA CCTTGCTGAG TGGAAATCAC TTGAATACTG TTCTACAGCC
 9101 AGTATAGACA GTGAGAACCC CCCAGACCTA AATAAAATCT GGAGTGAACC
 9151 ATTTTATCAG GAAACATATC TACCTTACAT GATCCGCAGC AAGCTGAAGC
 9201 TGCTGCTCCA GGGAGAGGCT GACCAGTCCC TGCTGACATT TATTGACAAA
 9251 GCTATGCACG GGGAGCTCCA GAAGGCGATT CTAGAGCTTC ATTACAGTCA
 9301 AGAGCTGAGT CTGCTTTACC TCCTGCAAGA TGATGTTGAC AGAGCCAAAT
 9351 ATTACATTCA AAATGGCATT CAGAGTTTTA TGCAGAATTA TTCTAGTATT
 9401 GATGTCCCTCT TACACCAAAG TAGACTCACC AAATTGCAGT CTGTACAGGC
 9451 TTTAACAGAA ATTGAGGAGT TCATCAGCTT TATAAGCAAA CAAGGCAATT
 9501 TATCATCTCA AGTTCCCTTT AAGAGACTTC TGAACACCTG GACAAACAGA
 9551 TATCCAGATG CTAAAATGGA CCCAATGAAC ATCTGGGATG ACATCATCAC
 9601 AAATCGATGT TTCTTTCTCA GCAAAATAGA GGAGAAGCTT ACCCCTCTTC
 9651 CAGAAGATAA TAGTATGAAT GTGGATCAAG ATGGAGACCC CAGTGACAGG
 9701 ATGGAAGTGC AAGAGCAGGA AGAAGATATC AGCTCCCTGA TCAGGAGTTG
 9751 CAAGTTTTTC ATGAAAATGA AGATGATAGA CAGTGCCCGG AAGCAGAAACA
 9801 ATTTCTCACT TGCTATGAAA CTACTGAAGG AGCTGCATAA AGAGTCAAAA
 9851 ACCAGAGACG ATTGGCTGGT GAGCTGGGTG CAGAGCTACT GCCGCCTGAG
 9901 CCACTGCCCG AGCCCGTCCC AGGGCTGCTC TGAGCAGGTG CTCACTGTGC
 9951 TGAAAACAGT CTCTTTGTTG GATGAGAACA ACGTGTCAAG CTACTTAARC
 10001 AAAAATATTC TGGCTTTCCG TGACCAGAAC ATTCTCTTGG GTACAACTTA
 10051 CAGGATCATA GCGAATGCTC TCAGCAGTGA GCCAGCCTGC CTTGCTGAAA

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Fig.10.

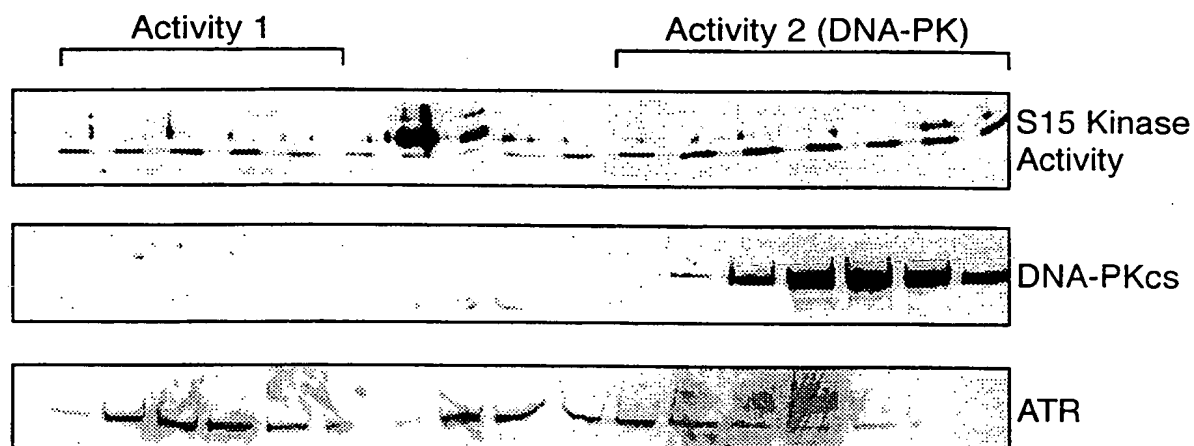


Fig.11.

